

NewSequence.txt
SEQUENCE LISTING

<110> CropDesign N.V.
<120> Monocotyledonous plants having improved growth characteristics and a method for making the same
<130> CD-097-PCT
<150> EP 03076719.8
<151> 2003-06-03
<160> 32
<170> PatentIn version 3.2
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<212> DNA
<213> Oryza sativa
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NewSequence.txt

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<212> PRT
<213> Oryza sativa
<400> 2

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20 25 30

Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
35 40 45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
50 55 60

Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser
65 70 75 80

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Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
85 90 95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile
100 105 110

Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser
115 120 125

Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp
130 135 140

Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser
145 150 155 160

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr
165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val
180 185 190

Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala
195 200 205

Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser
210 215 220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys
225 230 235 240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
245 250 255

Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu
260 265 270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala
290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val
305 310 315 320

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg

325

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330

335

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu
340 345 350

Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
355 360 365

Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
385 390 395 400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala
405 410 415

Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val
420 425 430

Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser
435 440 445

Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser
450 455 460

Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
465 470 475 480

Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His
485 490 495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
500 505 510

Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr
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Glu Gln Ser His Gly Gly Arg
530 535

<210> 3
<211> 1614

<212> DNA

<213> Arabidopsis thaliana

<400> 3

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NewSequence.txt

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<210> 4

<211> 538

<212> PRT

<213> *Arabidopsis thaliana*

<400> 4

Met Leu Asp Ser Leu Val Ser Lys Leu Pro Ser Leu Ser Thr Ser Asp
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NewSequence.txt

His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

NewSequence.txt

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
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Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
530 535

NewSequence.txt
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 <212> PRT
 <213> *Medicago sativa*
 <400> 6

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Thr Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu
 20 25 30

Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp
 35 40 45

Met Asn Glu Ser Ile Thr Ala Leu Leu Ile Gly Ile Cys Thr Gly Val
 50 55 60

Val Ile Leu Leu Phe Ser Gly Gly Lys Ser Ser His Ile Leu Val Phe
 65 70 75 80

Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
 85 90 95

Ala Gly Phe Gln Val Lys Lys Gln Phe Phe Val Asn Phe Met Thr
 100 105 110

Ile Thr Ser Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Val Ile Ile
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125

Thr Thr Gly Ala Thr Phe Ala Phe Lys Arg Met Asp Ile Gly Pro Leu
130 135 140

Glu Ile Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp
145 150 155 160

Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu
165 170 175

Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
180 185 190

Val Leu Phe Asn Ala Ile Gln Ser Phe Asp Leu Asn Gln Leu Asn Pro
195 200 205

Ser Ile Ala Leu His Phe Leu Gly Asn Phe Leu Tyr Leu Phe Val Ala
210 215 220

Ser Thr Leu Leu Gly Val Val Thr Gly Leu Leu Ser Ala Tyr Val Ile
225 230 235 240

Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu
245 250 255

Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Thr Tyr
260 265 270

Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His
275 280 285

Tyr Thr Trp His Asn Val Thr Gln Ser Ser Arg Ile Thr Thr Lys His
290 295 300

Ser Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu Tyr
305 310 315 320

Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp
325 330 335

Ser Pro Gly Thr Ser Ile Ala Ala Ser Ser Val Leu Leu Gly Leu Ile
340 345 350

Leu Leu Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
355 360 365

Leu Thr Lys Lys Ser Gln His Gln Lys Ile Ser Phe Arg Gln Gln Val
370 375 380

Ile Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu
385 390 395 400

Ala Tyr Asn Gln Phe Thr Met Ser Gly His Thr Gln Leu Arg Ser Asn
405 410 415

Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val
420 425 430

Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro His
435 440 445

Pro Lys Ile Thr Ser Ser Met Thr Thr Thr Glu Ser Thr Thr Pro Lys
450 455 460

Ser Phe Ile Val Pro Leu Leu Gly Asp Ser Arg Asp Ser Glu Ala Asp
465 470 475 480

Leu Glu Gly His Glu Ile His Arg Pro Asn Ser Leu Arg Ala Leu Leu
485 490 495

Ser Thr Pro Thr His Thr Val His Arg Leu Trp Arg Lys Phe Asp Asp
500 505 510

Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Val Glu
515 520 525

Pro Gly Ser Pro Ser Glu Arg Asn Gly Asn Gln Trp Gly
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<210> 7
<211> 2263
<212> DNA
<213> Suaeda maritima subsp. salsa

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gcacaaaagaa ataggtgaac aatgttgtca cagttgagct ctttttttgc aagtaagatg 180
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NewSequence.txt

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NewSequence.txt

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<211> 556
<212> PRT
<213> Suaeda maritima subsp. salsa

<400> 8

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20 25 30

Leu Leu Arg Gly Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg
35 40 45

Trp Met Asn Glu Ser Ile Thr Ala Leu Leu Ile Gly Leu Ser Thr Gly
50 55 60

Ile Ile Ile Leu Leu Ile Ser Gly Gly Lys Ser Ser His Leu Leu Val
65 70 75 80

Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe
85 90 95

Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile
100 105 110

Thr Ile Ile Leu Phe Gly Ala Val Gly Thr Leu Val Ser Phe Ile Ile
115 120 125

Ile Ser Leu Gly Ser Ile Ala Ile Phe Gln Lys Met Asp Ile Gly Ser
130 135 140

Leu Glu Leu Gly Asp Leu Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr
145 150 155 160

Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu
165 170 175

Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser
180 185 190

Val Val Leu Phe Asn Ala Ile Gln Asn Phe Asp Leu Thr His Ile Asp
195 200 205

His Arg Ile Ala Phe Gln Phe Gly Gly Asn Phe Leu Tyr Leu Phe Phe
210 215 220

NewSequence.txt

Ala Ser Thr Leu Leu Gly Ala Val Thr Gly Leu Leu Ser Ala Tyr Val
225 230 235 240

Ile Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala
245 250 255

Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe
260 265 270

Tyr Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser
275 280 285

His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys
290 295 300

His Ala Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu
305 310 315 320

Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Phe Val Ser
325 330 335

Asp Ser Pro Gly Thr Ser Val Ala Val Ser Ser Ile Leu Leu Gly Leu
340 345 350

His Met Val Gly Arg Ala Ala Phe Val Phe Pro Phe Ala Phe Leu Met
355 360 365

Asn Leu Ser Lys Lys Ser Asn Ser Glu Lys Val Thr Phe Asn Gln Gln
370 375 380

Ile Val Ile Trp Trp Ala Gly Leu Met Lys Ser Ala Val Ser Val Ala
385 390 395 400

Leu Ala Tyr Asn Gln Phe Ser Arg Ser Gly His Thr Gln Leu Arg Gly
405 410 415

Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr
420 425 430

Met Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Leu Phe Met Leu Pro
435 440 445

Gln Pro Lys His Phe Thr Ser Ala Ser Thr Val Ser Asp Leu Gly Ser
450 455 460

Pro Lys Ser Phe Ser Leu Pro Leu Leu Glu Asp Arg Gln Asp Ser Glu
465 470 475 480

NewSequence.txt

Ala Asp Leu Gly Asn Asp Asp Glu Glu Ala Tyr Pro Arg Gly Thr Ile
485 490 495

Ala Arg Pro Thr Ser Leu Arg Met Leu Leu Asn Ala Pro Thr His Thr
500 505 510

Val His His Tyr Trp Arg Arg Phe Asp Asp Tyr Phe Met Arg Pro Val
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<212> DNA
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NewSequence.txt

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taa						1623

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<211> 540

<212> PRT

<213> Zea mays

<400> 10

Met Gly Leu Gly Val Val Ala Glu Leu Val Arg Leu Gly Val Leu Ser
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Ser Thr Ser Asp His Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala
 20 25 30

Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg
 35 40 45

Trp Val Asn Glu Ser Thr Ala Leu Ile Val Gly Leu Gly Thr Gly Thr
 50 55 60

Val Ile Leu Met Ile Ser Arg Gly Val Val Ile His Val Leu Val Phe
 65 70 75 80

Ser Glu Asp Leu Phe Phe Tyr Leu Leu Pro Pro Ile Ile Phe Asn
 85 90 95

Ala Gly Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr
 100 105 110

Ile Thr Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Thr Val Ile
 115 120 125

Ser Leu Gly Ala Leu Gly Leu Ile Ser Arg Leu Asn Ile Gly Ala Leu
 130 135 140

NewSequence.txt

Glu Leu Gly Asp Tyr Leu Ala Leu Gly Ala Ile Phe Ser Ala Thr Asp
145 150 155 160

Ser Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Phe Leu
165 170 175

Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
180 185 190

Val Val Phe Asn Ala Leu Gln Asn Phe Asp Ile Thr His Ile Asp Ala
195 200 205

Glu Val Val Phe His Leu Leu Gly Asn Phe Phe Tyr Leu Phe Leu Leu
210 215 220

Ser Thr Val Leu Gly Val Ala Thr Gly Leu Ile Ser Ala Leu Val Ile
225 230 235 240

Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu
245 250 255

Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Ala
260 265 270

Leu Ser Gly Ile Leu Thr Val Phe Phe Gly Cys Ile Val Met Ser His
275 280 285

Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His
290 295 300

Ala Phe Ala Thr Leu Ser Phe Leu Ala Glu Thr Phe Leu Phe Leu Tyr
305 310 315 320

Val Gly Met Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp
325 330 335

Thr Pro Gly Lys Ser Leu Ala Ile Ser Ser Ile Leu Met Gly Leu Val
340 345 350

Met Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
355 360 365

Leu Ala Lys Lys Thr Glu His Glu Lys Ile Ser Trp Lys Gln Gln Val
370 375 380

Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu

385

390

NewSequence.txt
395

400

Ala Tyr Lys Lys Phe Thr Arg Ala Gly His Thr Gln Val Arg Gly Asn
 405 410 415

Ala Ile Met Ile Thr Ser Thr Ile Ile Val Val Leu Phe Ser Thr Met
 420 425 430

Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His
 435 440 445

Arg Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu
 450 455 460

His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Glu Pro
 465 470 475 480

Thr Asn Ile Pro Arg Pro Ser Ser Ile Arg Gly Glu Phe Leu Thr Met
 485 490 495

Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Ala Phe Met
 500 505 510

Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser
 515 520 525

Pro Thr Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
 530 535 540

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 <213> Zea mays

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NewSequence.txt

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cataggtact	ggagaaaaatt	tgtgacaaa	ttcatgcgcc	caatgttgg	cggcaggggc	1560
ttcgttaccct	tcgtccctgg	ttcaccaacg	gagaggaatc	cccacgatct	ttcgaageccc	1620
taa						1623

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 <212> PRT
 <213> Zea mays
 <400> 12

Met Gly Leu Gly Val Asp Ala Glu Thr Val Arg Leu Gly Val Leu Ser
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Ser Thr Ser Asp His Ala Ser Val Val Ser Asn Asn Phe Phe Val Ala
 20 25 30

Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg
 35 40 45

Met Val Asn Glu Ser Ile Thr Ala Leu Leu Val Gly Leu Gly Thr Gly
 50 55 60

Thr Val Ile Leu Met Ile Ser Arg Gly Val Ser Ile His Val Leu Val
 Page 19

65

70

NewSequence.txt

75

80

Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe
85 90 95

Asn Ala Gly Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Ile
100 105 110

Thr Ile Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile
115 120 125

Ile Ser Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro
130 135 140

Leu Glu Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr
145 150 155 160

Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu
165 170 175

Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser
180 185 190

Ile Val Val Phe Asn Ala Leu Gln Asn Phe Asp Ile Thr His Ile Asn
195 200 205

Ala Glu Val Val Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu
210 215 220

Leu Ser Thr Val Leu Gly Val Ala Thr Gly Leu Ile Ser Ala Leu Val
225 230 235 240

Ile Lys Lys Ile Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala
245 250 255

Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe
260 265 270

Ala Leu Ser Gly Ile Leu Thr Val Phe Phe Gly Cys Ile Val Met Ser
275 280 285

His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys
290 295 300

His Ala Phe Ala Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu
305 310 315 320

NewSequence.txt

Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Ser Val Ser
325 330 335

Asp Thr Pro Gly Lys Ser Ile Ala Ile Ser Ser Ile Leu Met Gly Leu
340 345 350

Val Met Leu Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser
355 360 365

Asn Leu Ala Lys Lys Asn Glu His Glu Lys Ile Ser Trp Lys Gln Gln
370 375 380

Val Val Ile Trp Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala
385 390 395 400

Leu Ala Tyr Asn Lys Phe Thr Arg Ala Gly His Thr Glu Val Arg Gly
405 410 415

Asn Glu Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr
420 425 430

Val Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Arg Leu Leu Met Pro
435 440 445

His Arg His Leu Thr Met Leu Ser Asp Asp Ser Thr Pro Lys Ser Leu
450 455 460

His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Ser Ile Glu Glu Pro
465 470 475 480

Thr Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Thr Thr Met
485 490 495

Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met
500 505 510

Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser
515 520 525

Pro Thr Glu Arg Asn Pro His Asp Leu Ser Lys Pro
530 535 540

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<211> 1620

<212> DNA

<213> Zea mays

<400> 13

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NewSequence.txt

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<210> 14
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 <212> PRT
 <213> Zea mays
 <400> 14

Met Ser Ile Gly Leu Thr Ala Glu Thr val Thr Asn Lys Leu Ala Ser
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NewSequence.txt

Ala Glu His Pro Gln Val Val Pro Asn Ser Val Phe Ile Ala Leu Leu
20 25 30

Cys Leu Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val
35 40 45

Asn Glu Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Thr Gly Thr Val
50 55 60

Ile Leu Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp
65 70 75 80

Glu Glu Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
85 90 95

Gly Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile
100 105 110

Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser
115 120 125

Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro Leu Glu
130 135 140

Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser
145 150 155 160

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr
165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val
180 185 190

Leu Phe Asn Ala Val Gln Lys Ile Asp Phe Glu His Leu Thr Gly Glu
195 200 205

Val Ala Leu Gln Val Phe Gly Asn Phe Leu Tyr Leu Phe Ser Thr Ser
210 215 220 225

Thr Val Leu Gly Ile Ala Thr Gly Leu Ile Thr Ala Phe Val Leu Lys
225 230 235 240

Thr Leu Tyr Phe Gly Arg His Ser Thr Thr Arg Glu Leu Ala Ile Met
245 250 255

Val Leu Met Ala Tyr Leu Ser Phe Met Leu Ala Glu Leu Phe Ser Leu
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260

NewSequence.txt

270

Ser Gly Ile Ile Thr Val Phe Phe Cys Gly Val Leu Met Ser His Val
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Ser Arg His Val
290 295 300

Phe Ala Met Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val
305 310 315 320

Gly Thr Asp Ala Leu Asp Phe Thr Lys Trp Lys Thr Ser Ser Leu Ser
325 330 335

Phe Gly Lys Ser Leu Gly Val Ser Ser Val Leu Leu Gly Leu Val Leu
340 345 350

Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
355 360 365

Ser Lys Lys His Pro Gly Glu Lys Ile Thr Ile Arg Gln Gln Val Val
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
385 390 395 400

Phe Asn Lys Phe Thr Arg Ala Gly His Thr Gln Val Arg Gly Asn Ala
405 410 415

Ile Met Ile Thr Ser Thr Ile Ile Val Val Leu Phe Ser Thr Val Val
420 425 430

Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His Arg
435 440 445

Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu His
450 455 460

Ser Pro Leu Leu Thr Ser Gln Leu Ile Ser Ser Ile Glu Glu Pro Thr
465 470 475 480

Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Met Thr Met Thr
485 490 495

Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met Arg
500 505 510

Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro
515 520 525

Thr Glu Arg Ser Ser Pro Asp Leu Ser Lys Ala
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<211> 1617
<212> DNA
<213> Zea mays

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NewSequence.txt

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<211> 538
<212> PRT
<213> Zea mays

<400> 16

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Asp His Ala Ser Val Val Ile Ile Thr Leu Phe Val Ala Leu Leu Cys
20 25 30

Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Leu Asn
35 40 45

Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Gly Thr Gly Val Val Ile
50 55 60

Leu Leu Ile Ser Arg Gly Lys Asn Ser Arg Leu Leu Val Phe Ser Glu
65 70 75 80

Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly
85 90 95

Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr
100 105 110

Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Leu
115 120 125

Gly Ala Ile Ala Thr Phe Ser Arg Met Ser Ile Gly Thr Leu Asp Val
130 135 140

Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val
145 150 155 160

Cys Thr Leu Gln Val Leu His Gln Asp Glu Thr Pro Phe Leu Tyr Ser
165 170 175

Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Leu
180 185 190

Phe Asn Ala Val Gln Lys Ile Gln Phe Thr His Ile Asn Ala Trp Thr
195 200 205

NewSequence.txt

Ala Leu Gln Leu Ile Gly Asn Phe Leu Tyr Leu Phe Ser Thr Ser Thr
210 215 220

Leu Leu Gly Ile Gly Thr Gly Leu Ile Thr Ala Phe Val Leu Lys Lys
225 230 235 240

Leu Tyr Phe Gly Arg His Ser Thr Thr Arg Glu Leu Ala Ile Met Ile
245 250 255

Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Ser Leu Ser
260 265 270

Gly Leu Leu Thr Val Phe Phe Cys Gly Val Leu Met Ser His Val Thr
275 280 285

Trp His Asn Val Thr Glu Ser Ser Arg Thr Thr Ser Arg His Val Phe
290 295 300

Ala Thr Leu Ser Phe Ile Ser Glu Thr Phe Ile Phe Leu Tyr Val Gly
305 310 315 320

Met Asp Ala Leu Asp Phe Glu Lys Trp Lys Thr Ser Ser Leu Ser Phe
325 330 335

Gly Gly Thr Leu Gly Val Ser Gly Val Leu Met Gly Leu Val Met Leu
340 345 350

Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala
355 360 365

Lys Lys His Gln Ser Glu Lys Ile Ser Phe Arg Met Gln Val Val Ile
370 375 380

Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Leu
385 390 395 400

Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile
405 410 415

Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe
420 425 430

Gly Met Ile Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly
435 440 445

His Pro Arg Glu Leu Ser Glu Pro Ser Ser Pro Lys Ser Phe His Ser
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450

455

NewSequence.txt

460

Pro Leu Leu Thr Ser Gln Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
 465 470 475 480

Ile Val Arg Pro Ser Ser Leu Arg Gly Leu Leu Thr Lys Pro Thr His
 485 490 495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
 500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
 515 520 525

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
 530 535

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 <213> Hordeum vulgare

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NewSequence.txt

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 <212> PRT
 <213> Hordeum vulgare
 <400> 18

Met Ala Phe Glu Val Val Ala Ala Gln Leu Ala Arg Leu Ser Asp Ala
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NewSequence.txt

Leu Ala Thr Ser Asp His Ala Ser Val Val Ser Ile Asn Leu Phe Val
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Ala Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn
35 40 45

Arg Trp Leu Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr
50 55 60

Gly Val Val Ile Leu Met Thr Thr Lys Gly Lys Ser Ser His Val Leu
65 70 75 80

Val Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile
85 90 95

Phe Asn Ala Gly Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe
100 105 110

Met Thr Ile Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe
115 120 125

Thr Ile Ser Leu Ala Ala Ile Ala Ile Phe Ser Lys Met Asn Ile Gly
130 135 140

Thr Leu Asp Val Ser Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala
145 150 155 160

Thr Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro
165 170 175

Phe Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr
180 185 190

Ser Val Val Leu Phe Asn Ala Leu Gln Asn Phe Asp Pro Asn Gln Ile
195 200 205

Asp Ala Ile Val Ile Leu Lys Phe Leu Gly Asn Phe Cys Tyr Leu Phe
210 215 220

Val Ser Ser Thr Phe Leu Gly Val Phe Ser Gly Leu Leu Ser Ala Tyr
225 230 235 240

Ile Ile Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val
245 250 255

Ala Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu
260 265 270

NewSequence.txt

Leu Asp Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met
275 280 285

Ser His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr
290 295 300

Lys His Ala Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe
305 310 315 320

Leu Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Ala
325 330 335

Ser Asp Ser Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly
340 345 350

Leu Val Leu Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu
355 360 365

Ser Asn Leu Thr Lys Lys Thr Glu Leu Glu Lys Ile Ser Trp Arg Gln
370 375 380

Gln Ile Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile
385 390 395 400

Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His
405 410 415

Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser
420 425 430

Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu
435 440 445

Pro Ala Ser Ser Asn Gly Asp Pro Ser Glu Pro Ser Ser Pro Lys Ser
450 455 460

Leu His Ser Pro Leu Leu Thr Ser Met Leu Gly Ser Asp Met Glu Ala
465 470 475 480

Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys
485 490 495

Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu
500 505 510

Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly
Page 31

515

520

NewSequence.txt
525Ser Pro Thr Asp Pro Asn Val Ile Val Ala
530 535

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 <211> 2422
 <212> DNA
 <213> Triticum aestivum
 <400> 19
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NewSequence.txt

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<211> 538

<212> PRT

<213> Triticum aestivum

<400> 20

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Leu Gly Thr Ser Asp His Ala Ser Val Val Ser Ile Thr Leu Phe Val
 20 25 30

Ala Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn
 35 40 45

Arg Trp Leu Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr
 50 55 60

Gly Val Val Ile Leu Met Thr Thr Lys Gly Lys Ser Ser His Val Leu
 65 70 75 80

Val Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile
 85 90 95

NewSequence.txt

Phe Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe
100 105 110

Met Ala Ile Thr Leu Phe Gly Ala Val Gly Thr Met Met Ser Phe Phe
115 120 125

Thr Ile Ser Leu Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly
130 135 140

Thr Leu Asp Val Ser Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala
145 150 155 160

Thr Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro
165 170 175

Phe Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr
180 185 190

Ser Val Val Leu Phe Asn Ala Leu Gln Asn Phe Asp Pro Asn Gln Ile
195 200 205

Asp Ala Ile Val Ile Leu Lys Phe Leu Gly Asn Phe Cys Tyr Leu Phe
210 215 220

Val Ser Ser Thr Phe Leu Gly Val Phe Thr Gly Leu Leu Ser Ala Tyr
225 230 235 240

Val Ile Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val
245 250 255

Ala Leu Val Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu
260 265 270

Leu Asp Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met
275 280 285

Ser His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr
290 295 300

Lys His Ala Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe
305 310 315 320

Leu Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Ala
325 330 335

Ser Asp Ser Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly
340 345 350

NewSequence.txt

Leu Val Leu Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu
 355 360 365

Ser Asn Leu Thr Lys Lys Thr Glu Leu Glu Lys Ile Ser Trp Arg Gln
 370 375 380

Gln Ile Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile
 385 390 395 400

Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His
 405 410 415

Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser
 420 425 430

Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu
 435 440 445

Pro Ala Ser Ser Asn Gly Ala Ala Ser Asp Pro Ala Ser Pro Lys Ser
 450 455 460

Leu His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Ala
 465 470 475 480

Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys
 485 490 495

Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu
 500 505 510

Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly
 515 520 525

Ser Pro Thr Asp Pro Asn Val Leu Val Glu
 530 535

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<211> 1726

<212> DNA

<213> Oryza sativa

<400> 21

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atcgggcacc tgctggaaagg gaaccggtgg gtcaatgaat ccatcaccgc gcttgtcatg 240

NewSequence.txt

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 <211> 544
 <212> PRT
 <213> Oryza sativa
 <400> 22

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NewSequence.txt

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20 25 30

Leu Cys Ser Cys Ile Val Ile Gly His Leu Leu Glu Gly Asn Arg Trp
35 40 45

Val Asn Glu Ser Ile Thr Ala Leu Val Met Gly Leu Ile Thr Gly Gly
50 55 60

Val Ile Leu Leu Val Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe
65 70 75 80

Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
85 90 95

Ala Gly Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Met Thr
100 105 110

Ile Ile Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Val Ile Ile
115 120 125

Ser Leu Gly Ala Met Thr Leu Phe Lys Lys Leu Asp Val Gly Pro Leu
130 135 140

Gln Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp
145 150 155 160

Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu
165 170 175

Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
180 185 190

Val Leu Phe Asn Ala Ile Glu Asp Ile Asp Ile Ala Asn Phe Asp Ser
195 200 205

Leu Val Leu Leu Ala Phe Ile Gly Asn Phe Leu Tyr Leu Phe Phe Thr
210 215 220

Ser Thr Leu Leu Gly Val Val Ala Gly Leu Leu Ser Ala Tyr Ile Ile
225 230 235 240

Lys Lys Leu Cys Phe Ala Arg His Ser Thr Asp Arg Glu Val Ala Ile
245 250 255

Met Ile Leu Met Ala Tyr Leu Ser Tyr Met Leu Ser Met Leu Leu Asp
260 265 270

NewSequence.txt

Leu Ser Gly Ile Leu Thr Val Phe Phe Ser Gly Ile Val Met Ser His
275 280 285

Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His
290 295 300

Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Leu Phe Leu Tyr
305 310 315 320

Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Leu Ala Ser Ser
325 330 335

Ser Pro Lys Lys Pro Ile Ala Leu Ser Ala Thr Ile Leu Gly Leu Val
340 345 350

Met Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
355 360 365

Leu Ser Lys Lys Glu Thr Arg Pro Lys Ile Ser Phe Lys Gln Gln Val
370 375 380

Ile Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu
385 390 395 400

Ala Tyr His Lys Phe Thr Ala Ser Gly His Thr Glu Leu Arg Ile Asn
405 410 415

Ala Ile Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met
420 425 430

Val Phe Gly Phe Phe Thr Lys Pro Leu Leu Asn Leu Leu Ile Pro Pro
435 440 445

Arg Pro Asp Ile Ala Ala Asp Leu Ser Ser Gln Ser Ile Ile Asp Pro
450 455 460

Leu Leu Gly Ser Leu Leu Gly Ser Asp Phe Asp Val Gly Gln Pro Ser
465 470 475 480

Pro Gln Asn Asn Leu Gln Leu Leu Leu Thr Ile Gln Thr Arg Ser Val
485 490 495

His Arg Val Trp Arg Lys Phe Asp Asp Arg Phe Met Arg Pro Met Phe
500 505 510

Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Val Glu Arg
515 520 525

NewSequence.txt

Ser Ile His Gly Ser Gln Leu Gly Thr Val Thr Glu Ala Glu His Ser
530 535 540

NewSequence.txt

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aatttgagag	ataaaactggg	aacaatctt	aattccgact	cacaatggtt	tcaaaatttt	1800
gatgaacagg	tattgaagcc	agtattcttg	gacaacgttt	ctccatcctt	acaagattcg	1860
gctacgcaat	cacctgcaga	tttctcttcc	caaaaccact	ag		1902

<210> 24

<211> 633

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

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Thr Ala Lys Arg Ala Val Asp Pro Asp Asp Asp Asp Glu Leu Leu Pro
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Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp
 35 40 45

Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu
 50 55 60

Phe Ile Met Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr
 65 70 75 80

Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile
 85 90 95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His
 100 105 110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val
 115 120 125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val
 130 135 140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly
 145 150 155 160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr
 165 170 175

NewSequence.txt

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser
180 185 190

Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile
195 200 205

Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly
210 215 220

Glu Ser Leu Leu Asn Asp Ala Ile Ser Ile Val Met Phe Glu Thr Cys
225 230 235 240

Gln Lys Phe His Gly Gln Pro Ala Thr Phe Ser Ser Val Phe Glu Gly
245 250 255

Ala Gly Leu Phe Leu Met Thr Phe Ser Val Ser Leu Leu Ile Gly Val
260 265 270

Leu Ile Gly Ile Leu Val Ala Leu Leu Leu Lys His Thr His Ile Arg
275 280 285

Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu
290 295 300

Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu
305 310 315 320

Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser
325 330 335

Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg
340 345 350

Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr
355 360 365

Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile
370 375 380

Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe
385 390 395 400

Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile
405 410 415

Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln
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420

NewSequence.txt
425

430

Met Met Thr Phe Trp Ala Gly Leu Arg Gly Ala Val Gly Val Ala Leu
435 440 445

Ala Leu Gly Ile Gln Gly Glu Tyr Lys Phe Thr Leu Leu Ala Thr Val
450 455 460

Leu Val Val Val Leu Thr Val Ile Ile Phe Gly Gly Thr Thr Ala
465 470 475 480

Gly Met Leu Glu Val Leu Asn Ile Lys Thr Gly Cys Ile Ser Glu Glu
485 490 495

Asp Thr Ser Asp Asp Glu Phe Asp Ile Glu Ala Pro Arg Ala Ile Asn
500 505 510

Leu Leu Asn Gly Ser Ser Ile Gln Thr Asp Leu Gly Pro Tyr Ser Asp
515 520 525

Asn Asn Ser Pro Asp Ile Ser Ile Asp Gln Phe Ala Val Ser Ser Asn
530 535 540

Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly
545 550 555 560

Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser
565 570 575

Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser
580 585 590

Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val
595 600 605

Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser
610 615 620

Pro Ala Asp Phe Ser Ser Gln Asn His
625 630

<210> 25

<211> 1857

<212> DNA

<213> Magnaporthe grisea

<400> 25

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NewSequence.txt

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tcaggccaa	
ttcttccggc	
acatcgaa	
aattctcacg	
ttcgcat	300
ttgcacgtt	
cctgtctgca	
gtagtcatcg	
gtgttatact	
atggcttac	
actcgctac	360
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gctcaccatg	
aactggatcg	
atgcccata	
tgtggcgca	
actttgtcag	420
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tgtcaccatc	
atagccatct	
tcaactcgta	
caaggtggac	
ccgaagctgt	480
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ctttggagag	
gccatcctca	
atgacgctgt	
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atcttcgagt	540
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aaggcagcgc	
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acacgtac	
caggagg	
ttttccca	720
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cttttcccag	
gccatacaca	780
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ttgttctg	
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caaacactat	
gcataactca	840
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agtacatgtt	
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tcgtccctc	
gcacaactgt	900
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agatcc	960
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<211> 618

NewSequence.txt

<212> PRT
<213> Magnaporthe grisea
<400> 26.

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Ala Glu Glu Pro Glu Pro Gly Gly Met Ala Val Gly Leu Ala Leu Arg
20 25 30

Val Phe Ala Val Asp Gly Leu Gln Asp Leu Val Ser Phe Asp Tyr Gln
35 40 45

Ile Phe Phe Asn Leu Leu Pro Pro Ile Ile Leu Ser Ser Gly Tyr
50 55 60

Glu Leu His Gln Ala Asn Phe Phe Arg His Ile Gly Thr Ile Leu Thr
65 70 75 80

Phe Ala Phe Ala Gly Thr Phe Leu Ser Ala Val Val Ile Gly Val Ile
85 90 95

Leu Trp Leu Tyr Thr Arg Val Pro Leu Glu Gly Leu Thr Met Asn Trp
100 105 110

Ile Asp Ala Ile Ser Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val
115 120 125

Thr Ile Ile Ala Ile Phe Asn Ser Tyr Lys Val Asp Pro Lys Leu Tyr
130 135 140

Thr Ile Ile Phe Gly Glu Ala Ile Leu Asn Asp Ala Val Ala Ile Val
145 150 155 160

Ile Phe Glu Ser Ala Gln Lys Ser Ala Arg Gly Leu Thr Lys Gly Ser
165 170 175

Ala Ala Gly Ile Ser Thr Phe Phe Trp Gly Phe Trp Ile Phe Leu Arg
180 185 190

Asp Phe Phe Gly Ser Leu Phe Ile Gly Ala Leu Leu Gly Ile Leu Thr
195 200 205

Ala Leu Met Leu Lys Tyr Thr Tyr Leu Arg Arg Phe Pro Lys Leu Glu
210 215 220

Ser Cys Leu Ile Val Leu Ile Ala Tyr Ala Thr Tyr Tyr Phe Ser Gln
225 230 235 240

NewSequence.txt

Ala Ile His Met Ser Gly Ile Val Ser Leu Leu Phe Cys Gly Ile Thr
245 250 255

Leu Lys His Tyr Ala Tyr Phe Asn Met Ser Arg Arg Thr Gln Leu Thr
260 265 270

Thr Lys Tyr Met Phe Gln Val Leu Ala Gln Leu Ser Glu Asn Phe Ile
275 280 285

Phe Ile Tyr Leu Gly Val Ser Leu Phe Thr Asp Lys Asp Leu Gln Phe
290 295 300

Gln Pro Leu Leu Ile Ile Val Thr Val Met Ala Val Cys Ala Ala Arg
305 310 315 320

Trp Val Ala Val Phe Pro Leu Ser Trp Ala Ile Asn Trp Phe His Lys
325 330 335

Tyr Arg Ala Glu Arg Arg Gly Ile Lys Asn Val Pro Glu Glu Leu Pro
340 345 350

Tyr Lys Tyr Gln Gly Met Leu Phe Trp Ala Gly Leu Arg Gly Ala Val
355 360 365

Gly Val Ala Leu Ala Ala Leu Leu Thr Ala Lys Asp His Arg Ala Phe
370 375 380

Lys Ala Thr Val Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly
385 390 395 400

Gly Thr Thr Val Asn Val Leu Glu Ile Leu Glu Ile Arg Thr Gly Val
405 410 415

Thr Asp Glu Ile Asp Ser Asp Asp Glu Phe Asp Ile Glu Ala Val Gly
420 425 430

Gly Tyr Tyr Lys Arg Ser Gly Asn Gly Ile Gly Tyr Ser Pro Ala Gly
435 440 445

Arg Asn Gly Val Val Pro Leu Asp Thr Arg Pro Gly Arg Arg Arg Asp
450 455 460

Ser Asn Gly Ala Val Gly Gly Arg Asp Ala Ser Gly Trp Ser Ser Gly
465 470 475 480

His Arg Ser Pro Leu Ser Ala Ala Arg Pro Gly Ser Leu Val Arg Thr
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485

NewSequence.txt
490

495

Gly Ser Thr Arg Glu Glu Ala Glu Arg Leu Asp Leu Leu Gly Asn Pro
 500 505 510

Gly Gly Ser Thr Asp Ser Asp Asp Phe Gly Ser Asp Ile Asp Thr Ser
 515 520 525

Asp Leu Pro Pro Pro Ala Pro Arg Arg Arg Ser Ser Pro Met Pro Pro
 530 535 540

Thr Gly Asp Glu Glu Ala Ala Gly Leu Pro Ala Gly Gly Ser Arg Thr
 545 550 555 560

Arg Ser Asn Thr Glu Thr Gly Gly Leu Ser Ala Thr Ala Ala Ile Arg
 565 570 575

Gln Leu Phe Ser Thr Glu Asp Pro Thr Ala Leu Phe Arg Gln Leu Asp
 580 585 590

Glu Asp Tyr Ile Lys Pro Lys Leu Leu Leu Asp Gly Gly Ala Gly Arg
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Gly Asn Gly Gly Ala Gly Gly Ser Ser
 610 615

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 <212> DNA
 <213> Oryza sativa

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 attgaaatttata tataatttcaa agagaataaa tccacatagc cgtaaagttc tacatgtgg 300
 gcattaccaa aatatataata gcttacaaaaa catgacaagc ttagtttggaa aaattgcaat 360
 ccttatcaca ttgacacata aagttagtga tgagtcataa tattattttc tttgttaccc 420
 atcatgtata tatgatagcc acaaaggatc tttgtatgtat atatcaaaga acatttttag 480
 gtgcaccaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540
 aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600
 aatcctcatac atccttcacc acaattcaaa tattatagtt gaagcatagt agta 654

NewSequence.txt

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gagagttccg ctccaccgtt ggacttgetc cgctgtcggc atccagaaaat tgcgtggcgg	720	
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NewSequence.txt

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<212> PRT
<213> artificial sequence

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<223> amiloride binding site

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Asp Val Phe Phe Leu Phe Leu Leu Pro Pro Ile
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<211> 10
<212> PRT
<213> artificial sequence

<220>
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<223> amiloride binding site

<400> 32
Phe Phe Xaa Xaa Leu Leu Pro Pro Ile Ile
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